

1110-0266P.ST25  
SEQUENCE LISTING

<110> NAGATA, Shigekazu et al.

<120> Novel Fas Ligand Derivative

<130> 1110-0266P

<140> 09/508,849

<141> 2000-03-17

<150> JP P1997-252541

<151> 1997-09-17

<160> 16

<170> PatentIn Ver. 2.1

<210> 1

<211> 258

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:amino acids at  
111-133 from N terminal are deleted from natural  
human Fas ligand

<400> 1

Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp  
1 5 10 15

Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys  
20 25 30

Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro  
35 40 45

Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro  
50 55 60

Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly  
65 70 75 80

Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly  
85 90 95

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Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Pro Ser  
100 105 110

Pro Pro Pro Glu Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly  
115 120 125

Lys Ser Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly  
130 135 140

Ile Val Leu Leu Ser Gly Val Lys Tyr Lys Gly Gly Leu Val Ile  
145 150 155 160

Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly  
165 170 175

Gln Ser Cys Asn Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn  
180 185 190

Ser Lys Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser  
195 200 205

Tyr Cys Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala  
210 215 220

Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu  
225 230 235 240

Leu Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr  
245 250 255

Lys Leu

<210> 2

<211> 277

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acids at  
128-131 from N terminal are deleted from natural  
human Fas ligand

<400> 2

Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp  
1 5 10 15

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Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys  
20 25 30

Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro  
35 40 45

Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro  
50 55 60

Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly  
65 70 75 80

Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly  
85 90 95

Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala  
100 105 110

Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Gly  
115 120 125

His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg Lys Val Ala His  
130 135 140

Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp  
145 150 155 160

Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly  
165 170 175

Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr  
180 185 190

Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser His Lys Val Tyr  
195 200 205

Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys  
210 215 220

Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr  
225 230 235 240

Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn  
245 250 255

Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe  
260 265 270

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Gly Leu Tyr Lys Leu  
275

<210> 3  
<211> 281  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:point mutation  
of a substitution of Lys 129 for Ala from N  
terminal is present in natural human Fas ligand  
<D6>

<400> 3  
Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp  
1 5 10 15  
Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys  
20 25 30  
Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro  
35 40 45  
Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro  
50 55 60  
Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly  
65 70 75 80  
Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly  
85 90 95  
Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala  
100 105 110  
Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu  
115 120 125  
Ala Gln Ile Gly His Pro Ser Pro Pro Glu Lys Lys Glu Leu Arg  
130 135 140  
Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu  
145 150 155 160  
Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr  
165 170 175

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Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr  
180 185 190

Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser  
195 200 205

His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met  
210 215 220

Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala  
225 230 235 240

Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His  
245 250 255

Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser  
260 265 270

Gln Thr Phe Phe Gly Leu Tyr Lys Leu  
275 280

<210> 4

<211> 774

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DNA coding for  
amino acids SEQ ID No.1

<400> 4

atgcagcagc cttcaatta cccatatccc cagatctact gggtgacag cagtgcac 60  
tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggct 120  
ggtaaaagga ggccaccacc accaccgcca ccgcccaccac taccacctcc gccgcccgg 180  
ccaccactgc ctccactacc gctgccaccc ctgaagaaga gagggaaacca cagcacaggc 240  
ctgtgtctcc ttgtgatgtt tttcatggtt ctgggtgcct tggtaggatt gggctgggg 300  
atgtttcagc tcttccaccc acagaaggag cccagtcac cccctgaaaa aaaggagctg 360  
aggaaaagtgg cccatctaacc aggcaagtcc aactcaaggt ccatgcctct ggaatggaa 420  
gacacctatg gaattgtcct gctttctgga gtgaagtata agaagggtgg ctttgtgatc 480

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aatgaaaactg ggctgtactt tgtatattcc aaagtatact tccggggtca atcttgcaac 540  
aacctgcccc tgagccacaa ggtctacatg aggaactcta agtatcccc gatatctgg 600  
atgatggagg ggaagatgat gagctactgc actactggc agatgtggc cccgagc 660  
tacctggggg cagtgttcaa tcttaccagt gctgatcatt tatatgtcaa cgtatctgag 720  
ctctctctgg tcaattttga ggaatctcag acgttttcg gcttatataa gctc 774

<210> 5  
<211> 831  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DNA coding for  
amino acids SEQ ID No.2

<400> 5  
atgcagcagc cttcaatta cccatatccc cagatctact ggggtggacag cagtgcac 60  
tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120  
ggtcaaagga ggccaccacc accaccgcca cggccaccac taccacctcc gccgcccgg 180  
ccaccactgc ctccactacc gctgccaccc ctgaagaaga gagggaaacca cagcacaggc 240  
ctgtgtctcc ttgtgatgtt tttcatggtt ctgggtgcct tggtaggatt gggctgggg 300  
atgttcagc tcttccaccc acagaaggag ctggcagaac tccgagagtc taccagccag 360  
atgcacacag catcatctt gggccacccc agtccacccc ctgaaaaaaaaa ggagctgagg 420  
aaagtggccc attaacagg caagtccaac tcaaggtcca tgcctctgga atggaaagac 480  
acctatggaa ttgtcctgct ttctggagtg aagtataaga aggggtggcct tgtgatcaat 540  
gaaactgggc tgtactttgt atattccaaa gtatacttcc ggggtcaatc ttgcaacaac 600  
ctgccccctga gccacaaggc ctacatgagg aactctaagt atccccagga tctggtgatg 660  
atggagggga agatgatgag ctactgcact actggcaga tgtggcccg cagcagctac 720  
ctggggcag tgttcaatct taccagtgct gatcattat atgtcaacgt atctgagctc 780

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tctctggtca atttttaggaa atctcagacg tttttcggt tatataagct c

831

<210> 6

<211> 843

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DNA coding for  
amino acids SEQ ID No.3

<400> 6

atgcagcagc cttcaatta cccatatccc cagatctact gggtggacag cagtgcgc 60

tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120

ggtaaaagga ggccaccacc accaccgcca ccgcccaccac taccacctcc gcccggccg 180

ccaccactgc ctccactacc gctgccaccc ctgaagaaga gagggAACCA cagcacaggc 240

ctgtgtctcc ttgtgatgtt tttcatgggt ctgggtgcct tggtaggatt gggctgggg 300

atgtttcagc tcttccaccc acagaaggag ctggcagaac tccgagagtc taccagccag 360

atgcacacag catcatctt ggaggcacaa ataggccacc ccagtccacc ccctgaaaaa 420

aaggagctga ggaaagtggc ccatttaaca ggcaagtcca actcaaggc catgcctctg 480

aatgggaag acacctatgg aattgtcctg ctttctggag tgaagtataa gaagggtggc 540

cttgcgtatca atgaaactgg gctgtacttt gtatattcca aagtatactt ccggggtaa 600

tcttgcaaca acctgcccct gagccacaag gtctacatga ggaactctaa gtatccccag 660

gatctggta tggatggaggga gaagatgatg agctactgca ctactggca gatgtgggc 720

cgcagcagct acctgggggc agtgttcaat cttaccagtg ctgatcattt atatgtcaac 780

gtatctgagc tctctctggc caattttaggaa gaatctcaga cgttttcgg cttatataag 840

ctc

843

<210> 7

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<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:a sense primer  
BOS6

<400> 7  
cctcagacag tggttcaaag 20

<210> 8  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:an antisense  
deletion primer DA4

<400> 8  
ttttcagggg gtggactggg ctccttctgt aggtggaag 39

<210> 9  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:HFLP3

<400> 9  
gctctagaac attctcggtg cctgtaac 28

<210> 10  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DA5

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<400> 10  
tggactgggg tggcccaaag atgatgctgt

30

<210> 11  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DA6

<400> 11  
gggggtggcct atttgtgcct ccaaagatga tgc

33

<210> 12  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:sequence of  
human FasL from amino acids 130 to137

<400> 12  
Gln Ile Gly His Pro Ser Pro Pro  
1 5

<210> 13  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:the amino acid  
sequence around the cleavage site of FasL

<400> 13  
Glu Lys Gln Ile  
1

<210> 14  
<211> 8

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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:the cleavage  
site of THN-alpha

<400> 14

Leu Ala Gln Ala Val Arg Ser Ser  
1 5

<210> 15

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:the cleavage  
site of CD40

<400> 15

Asn Ser Phe Glu Met Gln Lys Gly  
1 5

<210> 16

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:the cleavage  
site of FasL

<400> 16

Ser Leu Glu Lys Gln Ile Gly His  
1 5